

Could genetic diversity in eastern North Pacific gray whales reflect global historic abundance?

In Reply: Palsbøll *et al.* raise the possibility that our estimates of gray whale genetic diversity could reflect global diversity if a population of gray whales existed in the Southern Hemisphere. However, as they note, no evidence of gray whales has been discovered in the Southern Hemisphere. No fossils or subfossils have been reported, there are no accounts of this species from whaling records, and it is not known whether the specialized feeding requirements of gray whales could have been met in Southern Ocean areas. Although this lack of evidence does not eliminate the possibility of a gray whale population in the Southern Hemisphere, it does indicate a low probability that a large, widespread population existed there recently. In our paper on gray whale abundance before whaling (1), we use a new approach to evaluating “ghost” populations for their potential impact on the genetic diversity of current-day population diversity, as requested by the International Whaling Commission (2). Through a series of coalescent simulations, we specifically addressed the question posed by Palsbøll *et al.*: could a currently extinct population in the Atlantic have injected genetic diversity into the Pacific? Our simulations show that if the last major contact between Atlantic and Pacific populations occurred during the Sangamonian Interglacial period $\approx 140,000$ years ago, then the injection of genetic diversity probably would have eroded to low levels by now (Fig. 1). Clearly, direct genetic information from subfossil Atlantic gray whales would be better than our current indirect evidence, but until these data are available, our models suggest that measurements of genetic diversity in the Pacific are valid primarily for that ocean. Palsbøll *et al.* posit the possibility that a Southern Hemisphere gray whale population, which has never previously been proposed to our knowledge, served as a genetic conduit more recently than the Sangamonian Interglacial period. However, whales with Atlantic and Pacific populations that also have known Southern Ocean populations do not typically exhibit this genetic highway. Humpback whales in the North Pacific and Atlantic are genetically distinct, with only a few mtDNA lineages held in common (3). Common minke whales in the North Pacific, North Atlantic, and Southern Oceans are estimated to have diverged ≈ 1.5 mya, indicating that more recent migration events between these populations have been rare (4). In fin whales, data from California, Mexico, and the Mediterranean suggest strong genetic differences, despite a huge former population of this species in the Southern Ocean (5). In some cases, the traces of past interocean migration are seen in these data, but this migration is slow and does not homogenize these populations. Other whales, such as blue whales, are yet to be extensively studied and may show different patterns.

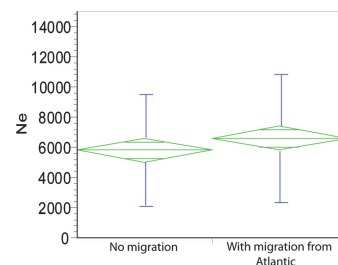
In addition, gray whales have a unique and specific feeding ecology that differs from all other species of baleen whale; unlike other species that feed in the water column, gray whales primarily rely on relatively shallow and highly productive benthic ecosystems (6). Although gray whales are capable of feeding in the water column as well, they are almost always observed feeding from the ocean floor and possess shorter baleen and modified mandible morphology that may be an adaptation to this divergent method of feeding (7). The existence of suitable benthic feeding grounds for gray whales in the Southern Hemisphere has not been ruled out, but this important difference between gray whales and

all other baleen whales provides a plausible explanation for why gray whale biogeography may differ substantially from other species. In our study, we stress the importance of exploring population structure and migration history in assessing effective population size from genetic data, and we used a simulation approach to better understand how different historical scenarios could impact genetic diversity in the modern eastern Pacific gray whale population. Although it may be impossible to gain perfect knowledge of populations that could have existed and migration between them, we believe that our approach provides a useful framework for determining the particular scenarios that could have substantial impacts on the results. These scenarios can then be investigated in light of empirical information about biogeographic and climatic history, and augmented by data from subfossil specimens. Until either simulation evidence or genetic data exist that reject this hypothesis, the most conservative interpretation of our data is that the levels of genetic diversity that we measured derive primarily from the North Pacific population of gray whales.

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Coalescent simulations of the increase in effective population size with migration from the Atlantic alone, when the effective population in the Atlantic is equivalent in size to that in the Pacific and migration ceases after the Sangamonian Interglacial period (114–131 kya). Mean diamonds indicate means (center lines), 95% confidence intervals around the means (top and bottom of diamonds), and standard deviation (error bars). Simulations were performed in SIMCOAL (8) (see ref. 1 for methods).

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The authors declare no conflict of interest.

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